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<!--StartFragment-->US-10-525-318-11
; Sequence 11, Application US/10525318
; Publication No. US20060112447A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Romano, Charles P
; APPLICANT: Bogdanova, Natalia N
; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression in
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15414)
; CURRENT APPLICATION NUMBER: US/10/525,318
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/407,428
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 5170
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fully synthetic expression cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(640)
; OTHER INFORMATION: P-e35S
; FEATURE:
; NAME/KEY: 5'UTL
; LOCATION: (665)..(735)
; OTHER INFORMATION: L-Ta.CAB
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (749)..(1239)
; OTHER INFORMATION: I-Os.ACT1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1241)..(4930)
; OTHER INFORMATION: Cry1Bb variant
; FEATURE:
; NAME/KEY: transcription_termination_sequence
; LOCATION: (4931)..(4936)
; OTHER INFORMATION: miscellaneous
; FEATURE:
; NAME/KEY: polyadenylation sequence
; LOCATION: (4937)..(5170)
; OTHER INFORMATION: T-Ta.hsp70
US-10-525-318-11

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Query Match          100.0%; Score 1797; DB 11; Length 5170;
Best Local Similarity 100.0%; Pred. No. 7.1e-142;
Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1247 ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG 1306

Qy      61 AACCCGTCCACCCAAATGAACCTGTCCCCGGACGCCCGCATCGAGGACTCCCTGTGCGTC 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1307 AACCCGTCCACCCAAATGAACCTGTCCCCGGACGCCCGCATCGAGGACTCCCTGTGCGTC 1366

Qy      121 GCGGAGGTCAACAACATCGACCCCTTCGTCTCCGCCTCCACGGTCCAGACGGGCATCAAC 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1367 GCGGAGGTCAACAACATCGACCCCTTCGTCTCCGCCTCCACGGTCCAGACGGGCATCAAC 1426

Qy      181 ATCGCTGGCGCATCCTCGGCGTCTGGGCGTCCCGTTTCGCTGGCCAGCTGGCCTCCTTC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1427 ATCGCTGGCGCATCCTCGGCGTCTGGGCGTCCCGTTTCGCTGGCCAGCTGGCCTCCTTC 1486

Qy      241 TACTCCTTCCTGGTCGGGGAGCTGTGGCCCTCCGGTCGCGACCCCTGGGAGATCTTCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1487 TACTCCTTCCTGGTCGGGGAGCTGTGGCCCTCCGGTCGCGACCCCTGGGAGATCTTCCTG 1546

Qy      301 GAGCACGTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1547 GAGCACGTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC 1606

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Qy	361	GCCCCGCTGGAGGGCCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG	420
Db	1607	GCCCCGCTGGAGGGCCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG	1666
Qy	421	CTGGACAACCGCAACGACGACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG	480
Db	1667	CTGGACAACCGCAACGACGACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG	1726
Qy	481	GAGCTGGACATCACCACCGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG	540
Db	1727	GAGCTGGACATCACCACCGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG	1786
Qy	541	CTCATGGTCTACGCCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG	600
Db	1787	CTCATGGTCTACGCCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG	1846
Qy	601	TTCCGCTCCGAGTGGGGCATGGCCTCGTCCGACGTCAACCAGTACTATCAGGAGCAGATC	660
Db	1847	TTCCGCTCCGAGTGGGGCATGGCCTCGTCCGACGTCAACCAGTACTATCAGGAGCAGATC	1906
Qy	661	CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCCTCAACAAC	720
Db	1907	CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCCTCAACAAC	1966
Qy	721	CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACAGTTCCGCCGCGACCTGACG	780
Db	1967	CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACAGTTCCGCCGCGACCTGACG	2026
Qy	781	CTGGGCGTCTGGACCTGGTCGCCTCTTCCCTCCTACGACACCCGCACCTACCCATC	840
Db	2027	CTGGGCGTCTGGACCTGGTCGCCTCTTCCCTCCTACGACACCCGCACCTACCCATC	2086
Qy	841	AACACGTCCGCCCAGCTGACCCGCGAGATCTACACCGACCCATCGGCCGACCAACGCT	900
Db	2087	AACACGTCCGCCCAGCTGACCCGCGAGATCTACACCGACCCATCGGCCGACCAACGCT	2146
Qy	901	CCCTCCGGCTTCGCGTCCACGAACTGGTTCAACAACAATGCCCGTCGTTCTCCGCCATC	960
Db	2147	CCCTCCGGCTTCGCGTCCACGAACTGGTTCAACAACAATGCCCGTCGTTCTCCGCCATC	2206
Qy	961	GAGGCTGCGATCTTCCGCCACCGCACCTCCTGGACTTCCCCGAGCAGCTGACCATCTAC	1020
Db	2207	GAGGCTGCGATCTTCCGCCACCGCACCTCCTGGACTTCCCCGAGCAGCTGACCATCTAC	2266
Qy	1021	TCCGCCTCGTCCCGCTGGTCGTCCACCCAGCACATGAACTACTGGGTGGGCCACCGCCTC	1080
Db	2267	TCCGCCTCGTCCCGCTGGTCGTCCACCCAGCACATGAACTACTGGGTGGGCCACCGCCTC	2326
Qy	1081	AACTTCAGGCCCATCGGTGGCACCTGAACACCTCCACCCAGGGCCTGACCAACAACACC	1140
Db	2327	AACTTCAGGCCCATCGGTGGCACCTGAACACCTCCACCCAGGGCCTGACCAACAACACC	2386
Qy	1141	TCCATCAACCCCGTCACCTCCAGTTCACGTCCCGCGACGTCTACCGACCGAGTCCAAC	1200
Db	2387	TCCATCAACCCCGTCACCTCCAGTTCACGTCCCGCGACGTCTACCGACCGAGTCCAAC	2446
Qy	1201	GCCGGCACCAACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC	1260
Db	2447	GCCGGCACCAACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC	2506
Qy	1261	TTCATCAACCCGCGAAGATCTACGAGCGTGGTGCGACCACTACTCCCAGCCGTACCAG	1320
Db	2507	TTCATCAACCCGCGAAGATCTACGAGCGTGGTGCGACCACTACTCCCAGCCGTACCAG	2566
Qy	1321	GGCGTGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT	1380
Db	2567	GGCGTGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT	2626
Qy	1381	CCCAACTACGAGTCTACTCCACCGCCTGTCCACATCGGCCTGATCATCGGCAACACC	1440
Db	2627	CCCAACTACGAGTCTACTCCACCGCCTGTCCACATCGGCCTGATCATCGGCAACACC	2686
Qy	1441	CTCAGGGCTCCCGTCTACTCCTGGACGACCGCTCCGCGGACCGACGAACACGATCGGT	1500
Db	2687	CTCAGGGCTCCCGTCTACTCCTGGACGACCGCTCCGCGGACCGACGAACACGATCGGT	2746

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Qy      1501 CCCAACCGCATCACCCAGATCCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC 1560
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Db      2747 CCCAACCGCATCACCCAGATCCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC 2806

Qy      1561 GTCGTGGGTGGCCAGGCTTCACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC 1620
         |||
Db      2807 GTCGTGGGTGGCCAGGCTTCACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC 2866

Qy      1621 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCCAGCGCTACCGCGTCCGCATC 1680
         |||
Db      2867 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCCAGCGCTACCGCGTCCGCATC 2926

Qy      1681 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 1740
         |||
Db      2927 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 2986

Qy      1741 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGTCTCTTC 1797
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Db      2987 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGTCTCTTC 3043

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RESULT 3

US-10-525-318-13

; Sequence 13, Application US/10525318

; Publication No. US20060112447A1

; GENERAL INFORMATION:

; APPLICANT: Monsanto Technology LLC

; APPLICANT: Romano, Charles P

; APPLICANT: Bogdanova, Natalia N

; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression in

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15414)

; CURRENT APPLICATION NUMBER: US/10/525,318

; CURRENT FILING DATE: 2005-02-23

; PRIOR APPLICATION NUMBER: 60/407,428

; PRIOR FILING DATE: 2002-08-29

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 5600

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: fully synthetic expression cassette

; FEATURE:

; NAME/KEY: promoter

; LOCATION: (26)..(640)

; OTHER INFORMATION: P-e35S

; FEATURE:

; NAME/KEY: 5'UTL

; LOCATION: (665)..(735)

; OTHER INFORMATION: L-Ta.CAB

; FEATURE:

; NAME/KEY: Intron

; LOCATION: (749)..(1239)

; OTHER INFORMATION: I-Os.ACT1

; FEATURE:

; NAME/KEY: Transit_peptide

; LOCATION: (1255)..(1401)

; OTHER INFORMATION: TP-Zm.rbcS

; FEATURE:

; NAME/KEY: Intron

; LOCATION: (1402)..(1564)

; OTHER INFORMATION: I-Zm.rbcS

; FEATURE:

; NAME/KEY: transit_peptide

; LOCATION: (1565)..(1651)

; OTHER INFORMATION: TP-Zm.rbcS

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1652)..(5341)

; OTHER INFORMATION: Cry1Bb variant

; FEATURE:

; NAME/KEY: transcription termination sequence

; LOCATION: (5342)..(5347)

; OTHER INFORMATION: miscellaneous

; FEATURE:
 ; NAME/KEY: polyadenylation sequence
 ; LOCATION: (5350)..(5592)
 ; OTHER INFORMATION: T-Os.LDH
 US-10-525-318-13

Query Match 100.0%; Score 1797; DB 11; Length 5600;
 Best Local Similarity 100.0%; Pred. No. 6.9e-142;
 Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG	60
Db	1658	ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG	1717
Qy	61	AACCGTCCACCCAAATGAACCTGTCCCGGACGCCCGCATCGAGGACTCCCTGTGCGTC	120
Db	1718	AACCGTCCACCCAAATGAACCTGTCCCGGACGCCCGCATCGAGGACTCCCTGTGCGTC	1777
Qy	121	GCGGAGGTCAACAACATCGACCCCTTCGTCTCCGCCTCCACGGTCCAGACGGGCATCAAC	180
Db	1778	GCGGAGGTCAACAACATCGACCCCTTCGTCTCCGCCTCCACGGTCCAGACGGGCATCAAC	1837
Qy	181	ATCGTGGCCGATCCTCGGCGTCTGGGCGTCCCGTTCGCTGGCCAGCTGGCCTCCTTC	240
Db	1838	ATCGTGGCCGATCCTCGGCGTCTGGGCGTCCCGTTCGCTGGCCAGCTGGCCTCCTTC	1897
Qy	241	TACTCCTTCTGGTGGGGAGCTGTGGCCCTCCGGTCCGACCCCTGGGAGATCTTCCTG	300
Db	1898	TACTCCTTCTGGTGGGGAGCTGTGGCCCTCCGGTCCGACCCCTGGGAGATCTTCCTG	1957
Qy	301	GAGCAGCTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC	360
Db	1958	GAGCAGCTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC	2017
Qy	361	GCCCGCTGGAGGGCCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG	420
Db	2018	GCCCGCTGGAGGGCCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG	2077
Qy	421	CTGGACAACCGCAACGACGACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG	480
Db	2078	CTGGACAACCGCAACGACGACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG	2137
Qy	481	GAGCTGGACATCACCACCGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG	540
Db	2138	GAGCTGGACATCACCACCGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG	2197
Qy	541	CTCATGGTCTACGCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG	600
Db	2198	CTCATGGTCTACGCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG	2257
Qy	601	TTCGGCTCCGAGTGGGGCATGGCCTCGTCCGACGTCAACCAGTACTATCAGGAGCAGATC	660
Db	2258	TTCGGCTCCGAGTGGGGCATGGCCTCGTCCGACGTCAACCAGTACTATCAGGAGCAGATC	2317
Qy	661	CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCCTCAACAAC	720
Db	2318	CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCCTCAACAAC	2377
Qy	721	CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACAGTTCGCGCGGACCTGACG	780
Db	2378	CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACAGTTCGCGCGGACCTGACG	2437
Qy	781	CTGGGCGTCTTGACCTGGTGCCTCTTCCCTCCTACGACACCCGCACCTACCCCATC	840
Db	2438	CTGGGCGTCTTGACCTGGTGCCTCTTCCCTCCTACGACACCCGCACCTACCCCATC	2497
Qy	841	AACAGTCCGCCCAGCTGACCCGCGAGATCTACACGACCCCATCGGCCGCACCAACGCT	900
Db	2498	AACAGTCCGCCCAGCTGACCCGCGAGATCTACACGACCCCATCGGCCGCACCAACGCT	2557
Qy	901	CCCTCCGGTTCGCGTCCACGAATGGTTCAACAACAATGCCCGTGTCTCCGCCATC	960
Db	2558	CCCTCCGGTTCGCGTCCACGAATGGTTCAACAACAATGCCCGTGTCTCCGCCATC	2617
Qy	961	GAGGCTGCGATCTTCCGCCACCGCACCTCTGGACTTCCCCGAGCAGCTGACCATCTAC	1020

Db 2618 GAGGCTGCGATCTTCGCCCCACCGCACCTCCTGGACTTCCCCGAGCAGCTGACCATCTAC 2677

Qy 1021 TCCGCCTCGTCCCGCTGGTTCGTCACCCAGCAGCATGAACTACTGGGTGGGCCACCGCCTC 1080
|||||

Db 2678 TCCGCCTCGTCCCGCTGGTTCGTCACCCAGCAGCATGAACTACTGGGTGGGCCACCGCCTC 2737

Qy 1081 AACTTCAGGCCCATCGGTGGCACCCCTGAACACCTCCACCCAGGGCCTGACCAACAACACC 1140
|||||

Db 2738 AACTTCAGGCCCATCGGTGGCACCCCTGAACACCTCCACCCAGGGCCTGACCAACAACACC 2797

Qy 1141 TCCATCAACCCCGTCACCTCCAGTTCACGTCCCGCGACGTCTACCGCACCGAGTCCAAC 1200
|||||

Db 2798 TCCATCAACCCCGTCACCTCCAGTTCACGTCCCGCGACGTCTACCGCACCGAGTCCAAC 2857

Qy 1201 GCCGGCACCAACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC 1260
|||||

Db 2858 GCCGGCACCAACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC 2917

Qy 1261 TTCATCAACCCCGCAGAATCTACGAGCGTGGTGGCACCACCTACTCCCAGCCGTACCAG 1320
|||||

Db 2918 TTCATCAACCCCGCAGAATCTACGAGCGTGGTGGCACCACCTACTCCCAGCCGTACCAG 2977

Qy 1321 GGCCTCGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT 1380
|||||

Db 2978 GGCCTCGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT 3037

Qy 1381 CCCAACTACGAGTCTACTCCCACCGCCTGTCCACATCGGCCTGATCATCGGCAACACC 1440
|||||

Db 3038 CCCAACTACGAGTCTACTCCCACCGCCTGTCCACATCGGCCTGATCATCGGCAACACC 3097

Qy 1441 CTCAGGGCTCCCGTCTACTCCTGGACGCACCGCTCCGCGGACCGCACGAACACGATCGGT 1500
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Db 3098 CTCAGGGCTCCCGTCTACTCCTGGACGCACCGCTCCGCGGACCGCACGAACACGATCGGT 3157

Qy 1501 CCCAACCGCATCACCCAGATCCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC 1560
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Db 3158 CCCAACCGCATCACCCAGATCCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC 3217

Qy 1561 GTCGTGGGTGGGCCAGGCTTACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC 1620
|||||

Db 3218 GTCGTGGGTGGGCCAGGCTTACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC 3277

Qy 1621 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCCAGCGCTACCGCGTCCGCATC 1680
|||||

Db 3278 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCCAGCGCTACCGCGTCCGCATC 3337

Qy 1681 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 1740
|||||

Db 3338 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 3397

Qy 1741 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGCTCCTTC 1797
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Db 3398 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGCTCCTTC 3454

RESULT 4

US-10-525-318-5

; Sequence 5, Application US/10525318

; Publication No. US20060112447A1

; GENERAL INFORMATION:

; APPLICANT: Monsanto Technology LLC

; APPLICANT: Romano, Charles P

; APPLICANT: Bogdanova, Natalia N

; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression in

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(15414)

; CURRENT APPLICATION NUMBER: US/10/525,318

; CURRENT FILING DATE: 2005-02-23

; PRIOR APPLICATION NUMBER: 60/407,428

; PRIOR FILING DATE: 2002-08-29

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 6600

; TYPE: DNA

; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: fully synthetic expression cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (174)..(490)
; OTHER INFORMATION: P-CAMV 35S
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (526)..(1320)
; OTHER INFORMATION: nptII
; FEATURE:
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (1315)..(1767)
; OTHER INFORMATION: T-AGRTu.nos3'
; FEATURE:
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (1325)..(1767)
; OTHER INFORMATION: T-AGRTu.nos3'
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1809)..(2386)
; OTHER INFORMATION: P-FMV
; FEATURE:
; NAME/KEY: 5' untranslated leader
; LOCATION: (2407)..(2480)
; OTHER INFORMATION: L-Os.betaTubulin
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (2498)..(2614)
; OTHER INFORMATION: I-Os.PAL
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2644)..(6333)
; OTHER INFORMATION: Cry1Bb variant
; FEATURE:
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (6345)..(6584)
; OTHER INFORMATION: T-Os.LDH
US-10-525-318-5

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Query Match 100.0%; Score 1797; DB 11; Length 6600;
 Best Local Similarity 100.0%; Pred. No. 6.5e-142;
 Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2650 ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG 2709

Qy      61  AACCCGTCACCCAAATGAACCTGTCCCCGGACGCCCGCATCGAGGACTCCCTGTGCGTC 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2710 AACCCGTCACCCAAATGAACCTGTCCCCGGACGCCCGCATCGAGGACTCCCTGTGCGTC 2769

Qy      121  GCGGAGGTCAACAACATCGACCCTTCGTCTCCGCCTCCACGGTCCAGACGGGCATCAAC 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2770 GCGGAGGTCAACAACATCGACCCTTCGTCTCCGCCTCCACGGTCCAGACGGGCATCAAC 2829

Qy      181  ATCGCTGGCCGCATCCTCGGCGTCTGGGCGTCCCGTTTCGCTGGCCAGCTGGCCTCCTTC 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2830 ATCGCTGGCCGCATCCTCGGCGTCTGGGCGTCCCGTTTCGCTGGCCAGCTGGCCTCCTTC 2889

Qy      241  TACTCCTTCCTGGTCGGGGAGCTGTGGCCCTCCGGTCGCGACCCCTGGGAGATCTTCCTG 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2890 TACTCCTTCCTGGTCGGGGAGCTGTGGCCCTCCGGTCGCGACCCCTGGGAGATCTTCCTG 2949

Qy      301  GAGCACGTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2950 GAGCACGTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC 3009

Qy      361  GCGCGCCTGGAGGGCCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3010 GCGCGCCTGGAGGGCCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG 3069

Qy      421  CTGGACAACCGCAACGACGCACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3070 CTGGACAACCGCAACGACGCACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG 3129

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Qy	481	GAGCTGGACATCACCACCGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG	540
Db	3130	GAGCTGGACATCACCACCGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG	3189
Qy	541	CTCATGGTCTACGCCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG	600
Db	3190	CTCATGGTCTACGCCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG	3249
Qy	601	TTCGGCTCCGAGTGGGGCATGGCCTCGTCCGACGTCAACCAGTACTATCAGGAGCAGATC	660
Db	3250	TTCGGCTCCGAGTGGGGCATGGCCTCGTCCGACGTCAACCAGTACTATCAGGAGCAGATC	3309
Qy	661	CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCTCAACAAC	720
Db	3310	CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCTCAACAAC	3369
Qy	721	CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACAGTTCCGCGCGACCTGACG	780
Db	3370	CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACAGTTCCGCGCGACCTGACG	3429
Qy	781	CTGGGCGTCTGGACCTGGTTCGCCTCTTCCCTCTACGACACCGCACCTACCCATC	840
Db	3430	CTGGGCGTCTGGACCTGGTTCGCCTCTTCCCTCTACGACACCGCACCTACCCATC	3489
Qy	841	AACACGTCCGCCCAGCTGACCCGCGAGATCTACACCGACCCCATCGGCGGCACCAACGCT	900
Db	3490	AACACGTCCGCCCAGCTGACCCGCGAGATCTACACCGACCCCATCGGCGGCACCAACGCT	3549
Qy	901	CCCTCCGGCTTCGCGTCCACGAACTGGTTCAACAACAATGCCCGTCGTTCTCCGCCATC	960
Db	3550	CCCTCCGGCTTCGCGTCCACGAACTGGTTCAACAACAATGCCCGTCGTTCTCCGCCATC	3609
Qy	961	GAGGCTGCGATCTTCCGCCCACCGCACCTCCTGGACTTCCCCGAGCAGCTGACCATCTAC	1020
Db	3610	GAGGCTGCGATCTTCCGCCCACCGCACCTCCTGGACTTCCCCGAGCAGCTGACCATCTAC	3669
Qy	1021	TCCGCCTCGTCCCGCTGGTCGTCACCCAGCAGATGAACTACTGGGTGGGCCACCGCCTC	1080
Db	3670	TCCGCCTCGTCCCGCTGGTCGTCACCCAGCAGATGAACTACTGGGTGGGCCACCGCCTC	3729
Qy	1081	AACTTCAGGCCATCGGTGGCACCCTGAACACCTCCACCCAGGGCCTGACCAACAACACC	1140
Db	3730	AACTTCAGGCCATCGGTGGCACCCTGAACACCTCCACCCAGGGCCTGACCAACAACACC	3789
Qy	1141	TCCATCAACCCCGTCACCTCCAGTTCACGTCCCGCGACGTCTACCGACCGAGTCCAAC	1200
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Qy	1201	GCCGGCACCACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC	1260
Db	3850	GCCGGCACCACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC	3909
Qy	1261	TTCATCAACCCGAGAACATCTACGAGCGTGGTGCGACCACCTACTCCCAGCCGTACCAG	1320
Db	3910	TTCATCAACCCGAGAACATCTACGAGCGTGGTGCGACCACCTACTCCCAGCCGTACCAG	3969
Qy	1321	GGCGTCGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT	1380
Db	3970	GGCGTCGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT	4029
Qy	1381	CCCAACTACGAGTCTACTCCCACCGCTGTCCACATCGGCCTGATCATCGGCAACACC	1440
Db	4030	CCCAACTACGAGTCTACTCCCACCGCTGTCCACATCGGCCTGATCATCGGCAACACC	4089
Qy	1441	CTCAGGGCTCCCGTCTACTCCTGGACGCACCGCTCCGCGGACCGACGAACACGATCGGT	1500
Db	4090	CTCAGGGCTCCCGTCTACTCCTGGACGCACCGCTCCGCGGACCGACGAACACGATCGGT	4149
Qy	1501	CCCAACCGCATCACCCAGATCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC	1560
Db	4150	CCCAACCGCATCACCCAGATCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC	4209
Qy	1561	GTCGTGGGTGGCCAGGCTTACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC	1620
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Qy      1621 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCCAGCGCTACCGCGTCCGCATC 1680
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Qy      1681 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 1740
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Qy      1741 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGCTCCTTC 1797
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RESULT 5

US-10-525-318-8

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; Sequence 8, Application US/10525318
; Publication No. US20060112447A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Romano, Charles P
; APPLICANT: Bogdanova, Natalia N
; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expression in
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15414)
; CURRENT APPLICATION NUMBER: US/10/525,318
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/407,428
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 7000
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fully synthetic expression cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (174)..(490)
; OTHER INFORMATION: P-CAMV 35S
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (526)..(1320)
; OTHER INFORMATION: nptII
; FEATURE:
; NAME/KEY: transcription termination & polyadenylation sequence
; LOCATION: (1325)..(1767)
; OTHER INFORMATION: T-AGRtu.nos3'
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1809)..(2386)
; OTHER INFORMATION: P-FMV
; FEATURE:
; NAME/KEY: 5'UTL
; LOCATION: (2407)..(2480)
; OTHER INFORMATION: L-Os.betaTUB
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (2498)..(2614)
; OTHER INFORMATION: I-Os.PAL
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (2644)..(2790)
; OTHER INFORMATION: TP-Zm.rbcs
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (2791)..(2953)
; OTHER INFORMATION: I-Zm.rbcs
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (2954)..(3040)
; OTHER INFORMATION: TP-Zm.rbcs
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3041)..(6730)
; . OTHER INFORMATION: Cry1Bb variant
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; FEATURE:
; NAME/KEY: transcription termination sequence
; LOCATION: (6731)..(6736)
; OTHER INFORMATION: miscellaneous sequence
; FEATURE:
; NAME/KEY: polyadenylation sequence
; LOCATION: (6742)..(6981)
; OTHER INFORMATION: T-Os.LDH
US-10-525-318-8

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Query Match          100.0%; Score 1797; DB 11; Length 7000;
Best Local Similarity 100.0%; Pred. No. 6.4e-142;
Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG 60
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Db      3047 ACCTCCAACCGCAAGAACGAGAATGAGATCATCAACGCCCTGTCGATCCCCACGGTCTCG 3106

Qy      61  AACCCGTCCACCCAAATGAACCTGTCCCGGACGCCGCATCGAGGACTCCCTGTGCGTC 120
          |||
Db      3107 AACCCGTCCACCCAAATGAACCTGTCCCGGACGCCGCATCGAGGACTCCCTGTGCGTC 3166

Qy      121  GCGGAGGTCAACAACATCGACCCCTTCGTCTCCGCTCCACGGTCCAGACGGGCATCAAC 180
          |||
Db      3167 GCGGAGGTCAACAACATCGACCCCTTCGTCTCCGCTCCACGGTCCAGACGGGCATCAAC 3226

Qy      181  ATCGTGGCGCATCCTCGGCGTCTGGGCGTCCCGTTCGCTGGCCAGCTGGCCTCCTTC 240
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Db      3227 ATCGTGGCGCATCCTCGGCGTCTGGGCGTCCCGTTCGCTGGCCAGCTGGCCTCCTTC 3286

Qy      241  TACTCCTTCTGGTGGGGAGCTGTGGCCCTCCGGTCGCGACCCCTGGGAGATCTTCCTG 300
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Qy      301  GAGCAGCTCGAGCAGCTCATCCGCCAGCAAGTCACCGAGAACACCCGCAACACGGCCATC 360
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Qy      361  GCGCCGCTGGAGGGGCTGGGCCGTGGCTACCGCTCCTACCAGCAGGCCCTGGAGACCTGG 420
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Qy      421  CTGGACAACCGCAACGACGACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG 480
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Db      3467 CTGGACAACCGCAACGACGACGCTCCCGCTCCATCATCCTGGAGCGCTACGTGGCGCTG 3526

Qy      481  GAGCTGGACATCACCAACGCCATCCCGCTCTTCCGCATCCGCAATGAAGAGGTGCCCTG 540
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Qy      541  CTCATGGTCTACGCCCAGGCTGCCAACCTGCACCTGCTCCTGCTTCGCGATGCATCCCTG 600
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Qy      661  CGCTACACCGAGGAGTACTCCAACCACTGCGTCCAGTGGTACAACACCGGCCTCAACAAC 720
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Qy      721  CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACCACTTCCGCCGCGACCTGACG 780
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Db      3767 CTGCGCGGCACGAACGCTGAGTCTGGCTGCGCTACAACCACTTCCGCCGCGACCTGACG 3826

Qy      781  CTGGGCGTCTGGACCTGGTCGCGCTCTTCCCTCCTACGACACCCGCACCTACCCCATC 840
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Db      3827 CTGGGCGTCTGGACCTGGTCGCGCTCTTCCCTCCTACGACACCCGCACCTACCCCATC 3886

Qy      841  AACACGTCCGCCAGCTGACCCGCGAGATCTACACCGACCCATCGGCCGCACCAACGCT 900
          |||
Db      3887 AACACGTCCGCCAGCTGACCCGCGAGATCTACACCGACCCATCGGCCGCACCAACGCT 3946

Qy      901  CCCTCCGGCTTCGCGTCCACGAACCTGGTTCAACAACAATGCCCGCTGCTTCTCCGCCATC 960
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Db 3947 CCCTCCGGCTTCGCGTCCACGAACTGGTTCAACAACAATGCCCCGTCGTTCTCCGCCATC 4006

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Qy 1021 TCCGCTCGTCCCGCTGGTCGTCCACCCAGCACATGAACTACTGGGTGGGCCACCGCCTC 1080
|||||

Db 4067 TCCGCTCGTCCCGCTGGTCGTCCACCCAGCACATGAACTACTGGGTGGGCCACCGCCTC 4126

Qy 1081 AACTTCAGGCCATCGGTGGCACCTGAACACCTCCACCCAGGGCCTGACCAACAACACC 1140
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Db 4127 AACTTCAGGCCATCGGTGGCACCTGAACACCTCCACCCAGGGCCTGACCAACAACACC 4186

Qy 1141 TCCATCAACCCCGTCAACCTCCAGTTCACGTCCCGCGACGTCTACCGCACCGAGTCCAAC 1200
|||||

Db 4187 TCCATCAACCCCGTCAACCTCCAGTTCACGTCCCGCGACGTCTACCGCACCGAGTCCAAC 4246

Qy 1201 GCCGGCACCAACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC 1260
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Db 4247 GCCGGCACCAACATCCTCTTCACGACCCCGGTCAACGGCGTCCCCTGGGCTCGCTTCAAC 4306

Qy 1261 TTCATCAACCCGCGAGAATCTACGAGCGTGGTGCGACCACTACTCCCAGCCGTACCAG 1320
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Db 4307 TTCATCAACCCGCGAGAATCTACGAGCGTGGTGCGACCACTACTCCCAGCCGTACCAG 4366

Qy 1321 GGCGTCGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT 1380
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Db 4367 GGCGTCGGCATCCAGCTCTTCGACTCCGAGACCGAGCTGCCACCCGAGACGACCGAGCGT 4426

Qy 1381 CCCAACTACGAGTCTACTCCCACCGCTGTCCACATCGGCCTGATCATCGGCAACACC 1440
|||||

Db 4427 CCCAACTACGAGTCTACTCCCACCGCTGTCCACATCGGCCTGATCATCGGCAACACC 4486

Qy 1441 CTCAGGGCTCCCGTCTACTCCTGGACGACCGCTCCGCGGACCGCACGAACACGATCGGT 1500
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Db 4487 CTCAGGGCTCCCGTCTACTCCTGGACGACCGCTCCGCGGACCGCACGAACACGATCGGT 4546

Qy 1501 CCCAACCGCATCACCCAGATCCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC 1560
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Db 4547 CCCAACCGCATCACCCAGATCCCCCTGGTCAAGGCCCTCAACCTGCACTCCGGCGTCACC 4606

Qy 1561 GTCGTGGGTGGCCAGGCTTCACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC 1620
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Db 4607 GTCGTGGGTGGCCAGGCTTCACCGGTGGCGACATCCTGCGCAGGACCAACACGGGCACC 4666

Qy 1621 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCAGCGCTACCGCGTCCGCATC 1680
|||||

Db 4667 TTCGGCGACATCCGCCTCAACATCAACGTCCCGCTGTCCAGCGCTACCGCGTCCGCATC 4726

Qy 1681 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 1740
|||||

Db 4727 CGCTACGCCTCCACGACCGACCTCCAGTTCTTCACGCGCATCAACGGCACCACGGTCAAC 4786

Qy 1741 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGTCTCTTC 1797
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Db 4787 ATCGGCAACTTCTCCCGCACCATGAACAGGGGCGACAACCTGGAGTACCGTCTCTTC 4843

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